

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:08:25 ; Search time 54.19 seconds
(without alignments)
345.504 Million cell updates/sec

Title: US-09-772-103-8
Perfect score: 655
Sequence: 1 MDFVQVIFSLISAVILS.....CQWSSYPLTFGGTKVEIK 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

al number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.invertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	436.5	66.6	108	4 Q9UL77	Q9ul77 homo sapien
2	428.5	63.4	108	4 Q9UL70	Q9ul70 homo sapien
3	417	63.7	107	4 Q9UL81	Q9ul81 homo sapien
4	411	62.7	106	5 Q9UL10	Q9ul10 schistosoma
5	410.5	62.7	108	4 Q9UL79	Q9ul79 homo sapien
6	387.5	59.2	298	11 Q9QYF0	Q9qyf0 mus musculu
7	387	59.1	109	4 Q9UL78	Q9ul78 homo sapien
8	386.5	59.0	107	11 Q9JL84	Q9jl84 mus musculu
9	379.5	57.9	214	11 Q9RIAS	Q9rlas mus musculu
10	375	57.3	109	4 Q9UL85	Q9ul85 mus musculu
11	372.5	56.9	97	11 Q9JL76	Q9jl76 mus musculu
12	364.5	55.6	108	4 Q9UL83	Q9ul83 homo sapien
13	361.5	55.2	101	11 Q9JL78	Q9jl78 mus musculu
14	361	55.1	109	4 Q9UL86	Q9ul86 homo sapien
15	341	52.1	238	11 Q99M37	Q99m37 mus musculu
16	326.5	49.8	107	11 Q9ERZ9	Q9erz9 mus musculu
17	321.5	49.1	99	11 Q9JL74	Q9jl74 mus musculu
18	319.5	48.8	103	11 Q9JL80	Q9jl80 mus musculu
19	309	47.2	104	11 Q9JL82	Q9jl82 mus musculu

20	297.5	45.4	114	4 Q9UL80	Q9ul80 homo sapien
21	294.5	45.0	109	6 Q9N0W5	Q9n0w5 oryctolagus
22	241	36.8	107	4 Q9NSD6	Q9nsd6 homo sapien
23	236.5	36.1	107	4 Q9UL82	Q9ul82 homo sapien
24	206	31.5	235	11 Q99M11	Q99m11 mus musculu
25	198	30.2	109	11 Q9ET13	Q9et13 mus musculu
26	189.5	28.9	130	4 Q9NP29	Q9np29 homo sapien
27	171.5	26.2	93	4 Q9UL76	Q9ul76 homo sapien
28	165	25.2	135	4 Q9H544	Q9h544 homo sapien
29	152.5	23.3	337	13 Q9IB02	Q9ib02 spherooides
30	142	21.7	334	13 Q9IB05	Q9ib05 spherooides
31	138.5	21.1	509	11 Q08907	Q08907 mus musculu
32	136.5	20.8	509	11 Q9QX57	Q9qx57 mus musculu
33	136.5	20.8	513	11 P97797	P97797 mus musculu
34	132.5	20.2	509	11 Q9WTN4	Q9wtN4 mus musculu
35	130.5	19.9	123	11 Q61243	Q61243 mus musculu
36	130.5	19.9	342	13 Q9IB00	Q9ib00 spherooides
37	125	19.1	122	4 Q99603	Q99603 homo sapien
38	125	19.1	137	4 Q9UDR1	Q9udr1 homo sapien
39	124.5	19.0	168	4 Q9UQ56	Q9uq56 homo sapien
40	121	18.5	122	4 Q99604	Q99604 homo sapien
41	121	18.5	509	11 Q9QW15	Q9qw15 rattus norv
42	117.5	17.9	140	13 Q9YHF9	Q9yhf9 ginglymosto
43	117.5	17.9	185	4 Q95775	Q95775 homo sapien
44	117.5	17.9	361	4 Q9HI05	Q9hiu5 homo sapien
45	117	17.9	503	4 P78324	P78324 homo sapien

ALIGNMENTS

RESULT 1
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN
CC EMBL; AF035037; AAD56273.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 66.6%; Score 436.5; DB 4; Length 108;
Best Local Similarity 82.2%; Pred. No. 9.3e-36;
Matches 88; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
QY 23 DIQMTQSPSSLSASVGRVITTCATSSI-TYMSWYQOKPKAPKLLIYDTNLSASVPS 81
|||||
Db 1 DIQMTQSPSSLSASVGRVITTCATSSI-TYMSWYQOKPKAPKLLIYDTNLSASVPS 60
|||||
QY 82 RFGSGSGTDTYLTISLQPEDFATYYCQWSSYPLTFGGTKVEIK 128

DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 53.7%; Score 417; DB 4; Length 107;
Best Local Similarity 79.4%; Pred. No. 7.7e-34;
Matches 85; Conservative 8; Mismatches 12; Indels 2; Gaps 2;

QY 23 DIQMTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPS 81
DQMTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPS 60
DQMTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPS 128
RFSGSGSGTDFTLTISLQPEDFATYYCQWSSYPLTFGGGKVEIK 106
RFSGSGSGTDFTLTISLQPEDFATYYCQWSSYPLTFGGGKVEIK 106

RESULT 4
Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
[1]
SEQUENCE FROM N.A.
RN Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RA "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum".
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL: AF207620; AAF19434.1; -.
DR HSSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 62.7%; Score 411; DB 5; Length 106;
Best Local Similarity 70.9%; Pred. No. 3e-33;
Matches 73; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 26 MTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPSRFSG 85
MTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPSRFSG 63
MTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPSRFSG 128
SGSGTDFTLTISLQPEDFATYYCQWSSYPLTFGGGKVEIK 106
SGSGTDFTLTISLQPEDFATYYCQWSSYPLTFGGGKVEIK 106

RESULT 5
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79

DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 53.7%; Score 417; DB 4; Length 107;
Best Local Similarity 79.4%; Pred. No. 7.7e-34;
Matches 85; Conservative 8; Mismatches 12; Indels 2; Gaps 2;

QY 23 DIQMTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPS 81
DQMTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPS 60
DQMTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPS 128
RFSGSGSGTDFTLTISLQPEDFATYYCQWSSYPLTFGGGKVEIK 106
RFSGSGSGTDFTLTISLQPEDFATYYCQWSSYPLTFGGGKVEIK 106

RESULT 4
Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
[1]
SEQUENCE FROM N.A.
RN Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RA "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum".
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL: AF207620; AAF19434.1; -.
DR HSSP: P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 62.7%; Score 411; DB 5; Length 106;
Best Local Similarity 70.9%; Pred. No. 3e-33;
Matches 73; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 26 MTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPSRFSG 85
MTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPSRFSG 63
MTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPSRFSG 128
SGSGTDFTLTISLQPEDFATYYCQWSSYPLTFGGGKVEIK 106
SGSGTDFTLTISLQPEDFATYYCQWSSYPLTFGGGKVEIK 106

RESULT 5
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79

DB 61 RESGSGTDFTLTISLQPEDFATYYCQWSSYPLTFGGGKVEIK 107
RESULT 2
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL: AF035044; AAD56280.1; -.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 65.4%; Score 428.5; DB 4; Length 108;
Best Local Similarity 78.5%; Pred. No. 5.7e-35;
Matches 84; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPS 81
DQMTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPS 60
DQMTQSPSSLSASVGRVITTCSSIT-YMSWYQKPGKAPKLLIYDTSNLSGVPS 128
RFSGSGSGTDFTLTISLQPEDFATYYCQWSSYPLTFGGGKVEIK 107
RFSGSGSGTDFTLTISLQPEDFATYYCQWSSYPLTFGGGKVEIK 107

RESULT 3
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL: AF035044; AAD56269.1; -.

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AC Q9UL79;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
EMBL; AF035035; AAD56271.1; -.
HSSP; P01607; IREL.
InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 108 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;

Query Match 62.7%; Score 410.5; DB 4; Length 108;
Best Local Similarity 75.7%; Pred. No. 3.4e-33;
Matches 81; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGDRTVITCSATSI--TYMSWYQKPGKAPKLLIYDTSNLSGVPS 81
Db 1 DIVMTQSPSSLSASVGDRTVITCSATSI--TYMSWYQKPGKAPKLLIYDTSNLSGVPS 81
QY 82 RFGSGSGTDTLTITSSLPQEDFATYCYQWSSYPLTFGGGKVEIK 128
Db 61 RFGSGSGTDTLTITSSLPQEDFATYCYQWSSYPLTFGGGKVEIK 107

RESULT 6
Q9QYF0
ID Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DE 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
CN 8 SCFV.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALE/C; TISSUE=SPLEEN;
RA Shiohara N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALE/C; TISSUE=SPLEEN;
RA Shiohara N., Demura T., Fukuda H.;
RT "Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a phage display subtraction
RT method.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
DR EMBL; AB036341; BAA88633.1; -.
DR HSSP; P01607; IREL.
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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 59.2%; Score 387.5; DB 11; Length 298;
Best Local Similarity 67.3%; Pred. No. 2e-30;
Matches 72; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGDRTVITCSATSI--TYMSWYQKPGKAPKLLIYDTSNLSGVPS 81
Db 173 DIETQSPASLSASVGTVTITCRASGNHNYLAWYQKQKSPQLLYNNAKTLDAGVPS 232
QY 82 RFGSGSGTDTLTITSSLPQEDFATYCYQWSSYPLTFGGGKVEIK 128
Db 233 RFGSGSGTQVSLKINSLPQEDFGSYCOHFMTPTPTFGGKLEIK 279

RESULT 7
Q9UL78
ID Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
EMBL; AF035036; AAD56272.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 109 109
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 59.1%; Score 387; DB 4; Length 109;
Best Local Similarity 65.7%; Pred. No. 7.1e-31;
Matches 71; Conservative 19; Mismatches 16; Indels 2; Gaps 1;

QY 23 DIQMTQSPSSLSASVGDRTVITCSATSI--TYMSWYQKPGKAPKLLIYDTSNLSGVPS 80
Db 1 EIVLTQSGTSLSPGERATLSCRASQSVSSYLAWYQKQKQAPRLIYGASSRATGIP 60
QY 81 SRFGSGSGTDTLTITSSLPQEDFATYCYQWSSYPLTFGGGKVEIK 128
Db 61 DRFGSGSGTDTLTITSLRLEDFEDCAVYCYQWSSYPLTFGGGKVEIK 108

RESULT 8
Q9JL84
ID Q9JL84 PRELIMINARY; PRT; 107 AA.
AC Q9JL84;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
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ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=BAIB/C;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis";
Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
EMBL; AF206022; AAF69320.1; -
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IgV; 1.
NON_TER 1 107
SEQUENCE 107 AA; 11648 MW; ACF9B1253ACALE5D CRC64;
Query Match 59.0%; Score 386.5; DB 11; Length 107;
Best Local Similarity 71.0%; Pred. No. 7.7e-31;
Matches 76; Conservative 11; Mismatches 19; Indels 1; Gaps
QY 23 DIQMTQSPSSLSASVGDRTVTCSTTSIT-YMSWYQQKPKAPKLLIYDTSNLASGVPS 81
Db 1 DIQMTQSTSLASGDGRVYXXXSASQISGNXXWFOQKPDGTVKLLIYYTSLXSGVPS 60
QY 82 RSGSGSGDYTLTISLQPEDFATYVQOQSSVPLTFGGGTKEIK 128
Db 61 RSGSGSGDYSLTISNLEPEDIATYVCOQYKSKPFTWFGGKTLEIK 107
RESULT 9
Q9RIA5 PRELIMINARY; PRT: 214 AA.
ID Q9RIA5
AC Q9RIA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
EMBL; AF152371; AAD40242.1; -
DR HSSP; P01789; IMCP.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IgV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
FT NON_TER 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
Query Match 57.9%; Score 379.5; DB 11; Length 214;

us-09-772-103-8.rspt

DR	SMART; SM00406; IGv; 1.
FT	NON_TER 1 1
FT	NON_TER 109 109
SO	SEQUENCE 109 AA; 119

Query Match 55.1%; Score 361; DB 4; Length 109;
Best Local Similarity 62.0%; Pred. NO. 2.6e-28;
Matches 67: Conservative 20; Mismatches 19; Indels

Qy		23	DIQWTQSPSSLSASVGDRTTTCSATSSI--TYMSWYQQPGKAPKLLIYDTSNLASGVP80 : : : :
n6		1	EIVITOSPCTISLPERGERATISCRAOSVSSTYLAWYOOKPGOAPRLIIYGTSSRATGIP60 : : : :

81 SRFSGSGGTDYTLTISSLOPEDFATYYCQOWSSYP LTFGGGTKVEIK 128

61 DBFSCSGSETDETI.TISRLEPDEFAWYCOOYGSSIFTEFGPGTKVDIK 108

RESULT 15

099M37 PRELIMINARY; PRT; 238 AA.

Q99K37: AC 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:5947).
DE

OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=MAMMARY TUMOR;

RA Strausberg R.;

Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases:

DR EMBL; BC002033; AA02033.1;
SO SEQUENCE 238 AA: 26344 MW:

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Query Match	52.1%	Score 341;	DB 11;	Length 238;
Best Local Similarity	57.4%	Pred. NO. 5.8e-26;		
Matches 66; Conservative	15;	Mismatches 28;	Indels 6;	Gaps 1;

QV 20 SRGDIOMTQSPSSLSASVGDRVTITCSATSSI-----TYMSWYQQKPGKAPKLLIYDTS 73

17 sssnvvmtotpi slpvsitgdoasiscr sssotivhsngntv lwylokpgospklltykvs 76

74 NLASGVPSRFSGGSGTDYTLTISSLOPEDFATYYCQWSSYP LTFGGGTKVEIK 128

DB 77 NRFGVDPFRFSGSGTGDTFLKISRVEAEDLGVIYCFQSGSHVPYTFGSGTKLEIK 131

1

Search completed: May 7, 2002, 12:08:26
Job time: 454 sec